

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 03:45:21 ; Search time 1604.32 Seconds  
(without alignments)  
9018.610 Million cell updates/sec

Title: US-09-811-118-2  
Perfect score: 1072  
Sequence: 1 GACCCGCCCACTCCGAC.....TTGCATCCACATGAAATTC 1072

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	964.8	90.0	1011	9	AL543692 AL543692
2	840.2	78.4	961	9	AL543655 AL543655
3	817.2	76.2	894	10	BI767772 BI767772
4	741.4	69.2	936	10	BI905842 BI905842
5	737.2	68.8	846	10	BI561449 BI561449
6	721.6	67.3	760	10	BI550170 BI550170
7	687.4	64.1	852	9	AL554204 AL554204
8	653.6	61.0	720	10	BI772530 BI772530
9	607	56.6	773	9	AL554203 AL554203
10	600.8	56.0	617	10	BE383506 BE383506
11	556.2	51.9	907	9	AL576668 AL576668
12	555.8	51.8	625	9	AW957082 AW957082
13	530.8	49.5	534	10	BE314194 BE314194
14	510.8	47.6	542	9	AW959644 AW959644
15	482.4	45.0	519	9	AA06605 AA06605
16	473.4	44.2	821	10	BF965615 BF965615
17					BF673639 BF673639

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c 19	457.6	42.7	1042	11	AK014199	AK014199 Mus muscu
c 20	453.4	42.3	466	9	AA599283	AA599283 ag35b03.s
c 21	452	42.2	466	9	AI635816	AI635816 t281c10.x
c 22	450.8	42.1	617	9	BB658193	BB658193 BB658193
c 23	449.8	42.0	678	9	AW142311	AW142311 EST292556
c 24	447.8	41.8	675	9	AW141464	AW141464 EST291514
c 25	447.4	41.7	466	9	AI332841	AI332841 qp96g11.x
c 26	446	41.6	464	9	AW576111	AW576111 UI-HF-BLO
c 27	441	41.1	562	9	AV602925	AV602925 AV602925
c 28	438	40.9	885	10	BI453803	BI453803 603175068
c 29	434.4	40.5	436	9	AA557291	AA557291 nt17b12.s
c 30	433.8	40.5	450	9	AA815259	AA815259 nt164d10.s
c 31	432.2	40.3	454	10	BE646653	BE646653 7e91h09.x
c 32	424.4	39.6	453	9	AI093865	AI093865 g93e01.s
c 33	423.4	39.5	436	9	AI094047	AI094047 g928f09.s
c 34	422.8	39.4	426	9	AA778372	AA778372 z156h05.s
c 35	415.8	38.8	419	9	AA777994	AA777994 z142c03.s
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c 41	391.2	36.5	547	9	AA749209	AA749209 ny11h09.s
c 42	387.6	36.2	399	9	AW236389	AW236389 x015e01.x
c 43	382.6	35.7	872	10	BI184046	BI184046 UNL-P-FN-
c 44	379.2	35.4	423	10	W47086	W47086 zc43e03.r1
c 45	377.4	35.2	524	10	BB856755	BB856755 7168c12.x

#### ALIGNMENTS

RESULT 1  
LOCUS AL543692 1011 bp mRNA linear EST 16-FEB-2001  
DEFINITION AL543692 LTI\_NFL006\_P12 Homo sapiens CDNA clone CS0DI006YD2 5  
prime, mRNA sequence.

ACCESSION AL543692  
VERSION AL543692.1 GI:12876171  
KEYWORDS EST.

#### SOURCE

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1011)  
AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.

TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.

#### FEATURES

source

1. 1011  
Location/Qualifiers

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/clone\_lib="LTI\_NFL006\_P12"  
/issue\_type="placenta"  
/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifestech.com URL :  
http://fulllength.invitrogen.com"

BASE COUNT 251 a 279 c 262 g 217 t 2 others  
ORIGIN

Query Match 90.0%; Score 964.8; DB 9; Length 1011;  
 Best Local Similarity 98.2%; Pred. No. 6.5e-227;  
 Matches 994; Conservative 2; Mismatches 14; Indels 2; Gaps 2;

QY 11 CCTCCGGAACCAAGCATGGTGGCGGCGAGCGGTGGCAGCGCGTGGCTGCTCTGTGGGCT 70  
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 QY 71 GCGGCGCTGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 130  
 DB 61 GCGGCGCTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 119  
 QY 131 AAATGTTGCTGGTGAAGAGTACCGCGATCGGTGCTGCTGTTGTAATGTGGCCAGC 190  
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 QY 191 GAGTGGGCTTCAACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 250  
 DB 180 GAGTGGGCTTCAACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 239  
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 QY 431 TCTGGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 490  
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 DB 480 GTAGGGGCTTGGAGCCCACTGTGTCTAGTGGAGAGGCTCAGACTCCAGATCAGAGCGCTC 539  
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 QY 671 GGAGAGACCACTGACT 730  
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 DB 780 CCATGAGAGGCTCTTGAGCAGTGAATCAGCAGCGATGAGAGTGTCTCCAAACAAAA 839  
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 DB 840 TGTGTGGCAATAGAGTATATCAGCAATATCTCCACCAAGGCTTCTGTAACTGG 899  
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 DB 900 GACCAATGATTACCTCAGAGGCTGTTGTAGAGATTAGATGAATACCTGTGAAGTGC 959  
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 LOCUS AL543655 L1L\_NFL006.PL2 Homo sapiens cDNA clone CSDD1006YD2 3  
 DEFINITION prime, mRNA sequence.  
 ACCESSION AL543655  
 VERSION AL543655  
 KEYWORDS GI:12876134  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 961)  
 AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
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 /note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@life.com URL : http://fulllength.invitrogen.com 4 others  
 BASE COUNT 231 a 207 c 252 g 267 t  
 ORIGIN

Query Match 78.4%; Score 840.2; DB 9; Length 961;  
 Best Local Similarity 99.0%; Pred. No. 3.2e-196;  
 Matches 864; Conservative 2; Mismatches 5; Indels 2; Gaps 2;

QY 201 TCACAGACCAAGCACTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 260  
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 QY 261 TCAACGTGCTGCGCTTCCCTGCAACCAAGTTGGCC-AACAGAGGCTGACAGCAACAG 319  
 DB 901 TCAACGTGCTGCGCTTCCCTGCAACCAAGTTGGCCMAACAGAGGAGGCTGACAGCAACAG 842  
 QY 320 GAGATTGAGAGCTTGGCTGCGGACCTACAGTGTCTCATTTCCCATGTTAGCAAGATT 379  
 DB 841 GAGATTGAGAGCTTGGCTGCGGACCTACAGTGTCTCATTTCCCATGTTAGCAAGATT 782  
 QY 380 GCAATGACCGGAGTGTGGTGGCCATCGGCTTCAAGTACCTGGGCGAGGAGTCTGGGAG 439  
 DB 781 GCAATGACCGGAGTGTGGTGGCCATCGGCTTCAAGTACCTGGGCGAGGAGTCTGGGAG 723  
 QY 440 GAGCCCACTGGAATCTTGAAGTACCTGTAAGTCCCAAGATGGAAGGAGTGTAGGAGGCT 499  
 DB 722 GAGCCCACTGGAATCTTGAAGTACCTGTAAGTCCCAAGATGGAAGGAGTGTAGGAGGCT 663  
 QY 500 TGGAGCCCAACTGTGTGAGTGGAGAGGAGTCAAGTCCAGATCAGAGGCTGTGAGGAG 559  
 DB 662 TGGAGCCCAACTGTGTGAGTGGAGAGGAGTCAAGTCCAGATCAGAGGCTGTGAGGAG 603  
 QY 560 CTATCTCTACTGAAGCAGAAAGTATTAAACACAGGAGTCTCTCTCTCAACAGGAGTATC 619  
 DB 602 CTATCTCTACTGAAGCAGAAAGTATTAAACACAGGAGTCTCTCTCTCAACAGGAGTATC 543



RESULT 4  
BI905842 936 bp mRNA linear EST 16-Oct-2001  
LOCUS 603062920F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5212085 5',  
DEFINITION mRNA sequence.  
ACCESSION BI905842  
VERSION BI905842.1 GI:16168433  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 936)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLML1532 row: h column: 06  
High quality sequence start: 5  
High quality sequence stop: 861.  
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cloning). Average insert size 1.7 kb, insert size range  
1.2-3.3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 027. Note:  
this is a NIH\_MGC Library."  
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Best Local Similarity 91.9%; Pred. No. 6.9e-172;  
Matches 854; Conservative 0; Mismatches 56; Indels 19; Gaps 6;  
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QY 73 GGCCTTGGCGGACGAGCAGGACTTCTACACTCAAGGGGTCACATCCGGGGCAA 132  
DB 69 GGCCTTGGCGGACGAGCAGGACTTCTACACTCAAGGGGTCACATCCGGGGCAA 128  
QY 133 ACTGGTGTGCTGGAGAATACCGCGGATCGGTGCTCTGTTGGTGAATGTGGCCAGCGA 192  
DB 129 ACTGGTGTGCTGGAGAATACCGCGGATCGGTGCTCTGTTGGTGAATGTGGCCAGCGA 188  
QY 193 GTGGCGCTTACAGACCACTACCGAGCCCTGCAGACAGCTGCAGCGAGAGCTGGGCC 252  
DB 189 GTGGCGCTTACAGACCACTACCGAGCCCTGCAGACAGCTGCAGCGAGAGCTGGGCC 248  
QY 253 CCACCACTTCAACGTGCTGGCTTCCCTGGCAACGATTGGCCACAGAGAGCTGACAG 312  
DB 249 CCACCACTTCAACGTGCTGGCTTCCCTGGCAACGATTGGCCACAGAGAGCTGACAG 308

QY 313 CAACAAGAGATGTGAGACTTTGGCTGGCCGACCTACAGTGTTCATTTCCCATGTTAG 372  
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QY 373 CAAGATTGCATTCACCGGTACTGTGTGCCATCTGCTTCAAGTACCTGGCCAGACTTC 432  
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QY 729 TGGGGGAAATTTCTAG---TATTTGATTTATTTGAATCTTACAGCAACAATAGGA 783  
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QY 784 ---CTCTGGCCATGAGAGCTCTT---GACCAGTGAATTCACGACGATACGAGCTG 836  
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DEFINITION mRNA sequence.  
ACCESSION BI561449  
VERSION BI561449.1 GI:15448763  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 846)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Mxios Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLML1755 row: m column: 08



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QY 361 CCCCATGTTTACGAAGATTGCAAGTACCGGTTACTGTGCCATCTCCCTTCAAGTACT 420
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RESULT 7
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LOCUS AL554204 L11_NFL006_P12 Homo sapiens cDNA clone CS0D1081YE05 5
DEFINITION prime, mRNA sequence.
ACCESSION AL554204
VERSION AL554204.1 GI:12894757
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 852)
            Li, W.B., Gruber, C., Jessee, J. and Polyes, D.
            Full-length cDNA libraries and normalization
            Unpublished (2001)
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segreife@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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/note="Vector: pCMVSPORT 6; Site-1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

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BASE COUNT 264 a 201 c 171 g 212 t 4 others
ORIGIN
Query Match 64 1% Score 687.4; DB 9; Length 852;
Best Local Similarity 99.3%; Pred. No. 1.3e-158;
Matches 688; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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QY 380 GCACTCACCGGTACTGTGGCCATCTGCTTCAAGTACCTGGCCCACTTCTGGGAAG 439
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Db 1 GCAGTACACGGTACTGTGGCCATCTGCTTCAAGTACCTGGCCCACTTCTGGGAAG 60
QY 440 GAGCCCACTGGAACCTTCTGGAAGTACTAGTACCCCAAGTGAAGGTGTAGGGGCT 499
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Db 61 GAGCCCACTGGAACCTTCTGGAAGTACTAGTACCCCAAGTGAAGGTGTAGGGGCT 120
QY 500 TGGGACCAACTGTGTGAGAGAGAGTCAAGTCAAGTCAAGGCGCTGAGAGAG 559
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Db 121 TGGGACCAACTGTGTGAGAGAGAGTCAAGTCAAGTCAAGGCGCTGAGAGAG 180
QY 560 CTCATCTACTGAGAGCAGAGACTTATTAACACCGCGTCTCTCTCCACCACTATC 619
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Db 181 CTCATCTACTGAGAGCAGAGACTTATTAACACCGCGTCTCTCTCCACCACTATC 240
QY 620 CCGGCCCACTGTGTGGGGCTGACCAATGCAAACTGCTTCAAAAGGAGAGACC 679
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Db 241 CCGGCCCACTGTGTGGGGCTGACCAATGCAAACTGCTTCAAAAGGAGAGACC 300
QY 680 CACTGACTCTCTCTCTCTCTCTTATGCAATGCTGCTTCTCTCTCTCTCTCTCTCTCT 739
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Db 301 CACTGACTCTCTCTCTCTCTCTTATGCAATGCTGCTTCTCTCTCTCTCTCTCTCTCT 360
QY 740 TTCTAGTATTTGATTTGAAATCTTACAGCAACAATAGAACCTCTGGCCAAATGAGA 799
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Db 361 TTCTAGTATTTGATTTGAAATCTTACAGCAACAATAGAACCTCTGGCCAAATGAGA 420
QY 800 GCTCTGACCAAGTAATACACACCGCCATAGAACGCTTCCCAACAAAATGTGTGCCA 859
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Db 421 GCTCTGACCAAGTAATACACACCGCCATAGAACGCTTCCCAACAAAATGTGTGCCA 480
QY 860 ATAGAAGTATATCAAGCAATAATCTCCACCAAGGCTTGTAAACTGGGACCAATGAT 919
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Db 481 ATAGAAGTATATCAAGCAATAATCTCCACCAAGGCTTGTAAACTGGGACCAATGAT 540
QY 920 TACCTCATAGGCTGTTGTGAGAGATTAGATGAATACCTGTGAAGTGTGAGCAGTG 979
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Db 541 TACCTCATAGGCTGTTGTGAGAGATTAGATGAATACCTGTGAAGTGTGAGCAGTG 600
QY 980 CCAAGCAATAGAGAGGATTCATGAACATTTTTCATATTAACCAAAAATTAATCTTG 1039
    |||||||
Db 601 CCAAGCAATAGAGAGGATTCATGAACATTTTTCATATTAACCAAAAATTAATCTTG 660
QY 1040 TATCAATTAATAAATCTGCATCCACATGAATTTTC 1072
    |||||||
Db 661 TATCAATTAATAAATCTGCATCCACATGAATTTTC 693
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RESULT 8
BI772530 720 bp mRNA linear EST 25-SEP-2001
LOCUS BI772530
DEFINITION 60305444F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5204003 5',
            mRNA sequence.
ACCESSION BI772530

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VERSION      B1772530.1 GI:15764108
KEYWORDS
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 720)
              NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE        Unpublished (1999)
JOURNAL
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgaps-remail.nih.gov
              Tissue Procurement: Life Technologies, Inc.
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: L1M1511 row: 9 column: 12
              High quality sequence start: 4
              High quality sequence stop: 719.
              Location/Qualifiers
                1..720
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:5204003"
                /clone_lib="NIH_MGC_122"
                /lab_host="DH10B"
                /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
                Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
                anonymous pool of 24 week female lung, 16 week female
                spleen, and 20-22 week male spleens. Library is oligo-dT
                primed and directionally cloned (EcoRV site is destroyed
                upon cloning). Average insert size 1.4 kb, insert size
                range 1-3 kb. Library is normalized and enriched for
                full-length clones and was constructed by C. Gruber
                (Invitrogen). Research Genetics tracking code 026. Note:
                this is a NIH-MGC Library."
BASE COUNT   150 a 225 c 204 g 141 t
ORIGIN
Query Match   61.0%; Score 653.6; DB 10; Length 720;
Best Local Similarity 98.8%; Pred. No. 2.7e-150;
Matches 711; Conservative 0; Mismatches 4; Indels 5; Gaps 5;

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Db 361 CCATGTTTACGAGATTGCTACCGGCTACGTCGCCATCTGCTCAAGTACT 420
Qy 421 GGCCAGACTTCTGGGAG-GAGCCACCTGGAACTTGTGAATCACTAGTAGCCCGAG 479
Db 421 GGCCAGACTTCTGGGAGTGAATGAGCCAGCTGAACTTGTGAATCACTAGTAGCCCGAG 480
Qy 480 ATGG-AAAGGTGTAGGGGCTTGGACCCAACTGTGTGTCAGTGAAGAGTCAAGTCCAG 538
Db 481 ATGGTAAAGTGTAGGGGCTTGGACCCAACTGTGTGTCAGTGAAGAGTCAAGTCCAG 540
Qy 539 ATCAGAGCCCTGTGTGAGAGAGCTCATCTCTACTGAAACGAGAACTTATACACCGCT 598
Db 541 ATCAGAGCCCTGTGTGAGAGAGCTCATCTCTACTGAAACGAGAACTTATACACCGCT 600
Qy 599 CTCCTCTCCACACCTCATCTCCGCGCCACTGTGTGGGCTGACCAATGCAATCAAT 658
Db 601 CTCCTCTCCACACCTCATCTCCGCGCCACTGTGTGGGCTGACCAATGCAATCAAT 660
Qy 659 GGTGCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 718
Db 661 GGTGCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

RESULT 9
AL554203 773 bp mRNA linear EST 16-FEB-2001
LOCUS AL554203 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0D1081YE05 3
DEFINITION prime, mRNA sequence.
ACCESSION AL554203.1 GI:12894755
VERSION AL554203
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 773)
              Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
              Full-length cDNA libraries and normalization
              Unpublished (2001)
AUTHORS      Genoscope
TITLE        Genoscope - Centre National de Sequencage
JOURNAL      BP 191 91006 Evry cedex - France
              Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
COMMENT      Location/Qualifiers
                1..773
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="CS0D1081YE05"
                /clone_lib="LTI_NFL006_PL2"
                /tissue_type="placenta"
                /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                was primed with a NotI-oligo(dT) primer. Five prime end
                enriched, double-stranded cDNA was digested with Not I and
                cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                vector. Library was normalized. Library was constructed by
                Life Technologies. Contact : Feng Liang Life Technologies,
                a division of Invitrogen 9800 Medical Center Drive
                Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                Email : fliang@lifestech.com URL :
                http://fulllength.invitrogen.com
BASE COUNT   182 a 151 c 216 g 204 t 20 others
ORIGIN
Query Match   56.6%; Score 607; DB 9; Length 773;
Best Local Similarity 90.6%; Pred. No. 8.3e-139;
Matches 628; Conservative 12; Mismatches 53; Indels 0; Gaps 0;

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Db 713 GAGCCCMCTGGAACCTCTGGAAGTACCTAGTAGGCCCMAGATGGAAGGTGGAAGGGCT 654
QY 500 TGGAGCCCAACTGTGTGAGTGGAGAGGAGTCACTCCAGATACACAGCGCTGTGAGGAAG 559
Db 653 TGGAAACCCMACTGTTTATGAGGAGAGANTCAKACCCAGATMACTGTGTGAGTAAG 594
QY 560 CTATCTCTACTGGAAGCAGAGAAGACTTATTAACCAACCGCGTCCCTCCACCACTCATC 619
Db 593 CTATCTCTACTGGAAGCAGAGACACTATCTACACACCGCTCCCTCCACCACTCTCTC 534
QY 620 CCGCCCACTGTGTGGGGGTGACCAATGCAAACTCAATGTGTCTTCAAGAGGAGAC 679
Db 533 CCGCCCACTGTGTGGGGGTGACCAACGACACTCCACTGTGTCTTCAAGAGCAGACAC 474
QY 680 CACTGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 739
Db 473 CACTGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 414
QY 740 TTCTAGTATTTTGTATTTGATTTGAATCTTACAGCAAAATAGAACTCTGCGCAATGAGA 799
Db 413 TTCTAGTATTTTGTATTTGATTTGAATCTTACAGCAAAATAGAACTCTGCGCAATGAGA 354
QY 800 GCTCTTGACCACTGATTCACCAACCGATACGAACGCTCTGCAACAAAATGTGTGGCAA 859
Db 353 GCTCTTGACCACTGATTCACCAACCGATACGAACGCTCTGCAACAAAATGTGTGGCAA 294
QY 860 ATGAGATATATATCAAGCAATATCTCCACCCCAAGGCTTGTAACTGGGAGACATGAT 919
Db 293 ATGAGATATATATCAAGCAATATCTCCACCCCAAGGCTTGTAACTGGGAGACATGAT 234
QY 920 TACCTCATAGAGGCTGTGTGAGAGATTAGAGTGAATACCTGTGAAGTGGCTAGGAGAGT 979
Db 233 TACCTCATAGAGGCTGTGTGAGAGATTAGAGTGAATACCTGTGTGAAGTGGCTAGGAGAGT 174
QY 980 CCAAGCAATAGAGAGGATTCATGAACTTTTGTGATTAACCAAAAAATTAACCTGT 1039
Db 173 CCAAGCAATAGAGAGGATTCATGAACTTTTGTGATTAACCAAAAAATTAACCTGT 114
QY 1040 TATCAATAAAAAAGCTGATCCATCAACATGAATTC 1072
Db 113 TATCAATAAAAAAGCTGATCCATCAACATGAATTC 81

RESULT 10
LOCUS BE383506 617 bp mRNA linear EST 21-JUL-2000
DEFINITION 601298586f1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628580 5',
VERSION BE383506 mRNA sequence.
KEYWORDS BE383506.1 GI:9328871
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 617)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: L1CM313 row: 1 column: 21
High quality sequence start: 7
High quality sequence stop: 617.
Location/Qualifiers
1..617
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/db_xref="taxon:9606"
/clone="IMAGE:3628580"
/clone_1b="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

BASE COUNT 130 a 193 c 178 g 116 t
ORIGIN

Query Match 56.0%; Score 600.8; DB 10; Length 617;
Best local similarity 99.7%; Pred. No. 2.6e-137;
Matches 602; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 46 AGCGGCGTGGCTGCTCTCTGTGGGCTGCGGCTGCGGACAGACAGACTTTCAGCA 105
Db 14 AGCGGCGTGGCTGCTCTGTGGGCTGCGGCTGCGGACAGACAGACTTTCAGCA 73
QY 106 CTTCAGAGGGGTCAACATCCGGGGCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 165
Db 74 CTTCAGAGGGGTCAACATCCGGGGCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 133
QY 166 GTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 225
Db 134 GTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 193
QY 226 GCAGCAGCTGTGACGAGACCTGGGCCCCCACTTCAAGTGTGTGTGTGTGTGTGTGT 285
Db 194 GCAGCAGCTGTGACGAGACCTGGGCCCCCACTTCAAGTGTGTGTGTGTGTGTGTGT 253
QY 286 CCAAGTTGGCCAAACAGAGAGCTGTGACGAAAGAGATTTGAGAGTGGCTTCCGCGCAC 345
Db 254 CCAAGTTGGCCAAACAGAGAGCTGTGACGAAAGAGATTTGAGAGTGGCTTCCGCGCAC 313
QY 346 CTACAGTGTCTATTCCTCCATGTTTGAAGATTTGACAGTACCGGTACTGTGCCATCC 405
Db 314 CTACAGTGTCTATTCCTCCATGTTTGAAGATTTGACAGTACCGGTACTGTGCCATCC 373
QY 406 TGCCTTCAAGTACCTGTGGCCCACTTCTGTGGAAGAGCCACCTGTGAACTTGTGAAGTA 465
Db 374 TGCCTTCAAGTACCTGTGGCCCACTTCTGTGGAAGAGCCACCTGTGAACTTGTGAAGTA 433
QY 466 CCTAGTAGCCCGAGATGGAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 525
Db 434 CCTAGTAGCCCGAGATGGAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 493
QY 526 GGTTCAGACTTCAGATACACAGCGCTGTGAGAGAGTCACTTACTGAAAGGAGACTT 585
Db 494 GGTTCAGACTTCAGATACACAGCGCTGTGAGAGAGTCACTTACTGAAAGGAGACTT 553
QY 586 ATACACACCGGCTGTCTCTCTCACACACTGTATCCCGCCACCTGTGTGTGTGTGTGT 645
Db 554 ATACACACCGGCTGTCTCTCTCACACACTGTATCCCGCCACCTGTGTGTGTGTGTGT 613
QY 646 TGCA 649
Db 614 TGCA 617

RESULT 11
LOCUS AL576668 907 bp mRNA linear EST 16-FEB-2001
DEFINITION AL576668 L1.NFL006.P12 Homo sapiens cDNA clone CS0D10807K02 3
prime, mRNA sequence.
ACCESSION AL576668
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VERSION		AL576668.1	GI:12939038
KEYWORDS		EST.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
TITLE		1 (bases 1 to 907)	
JOURNAL		L.I.W.B., Gruber.C., Jesse,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)	
COMMENT		Contact : Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.  Location/Qualifiers	
FEATURES		Source	
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		/clone="CSODI080KK02"	
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		/tissue_type="placenta"	
		/note="Vector: pCMVSPORT 6; Site.1: NotI; 1st strand cDNA was primed with a NotI-Oligo(gt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library has constructed by Life Technologies. Contact : Feng Liang Life Technologies a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"	
BASE COUNT		309 a	88 c 219 g 251 t 40 others
ORIGIN			
		Query Match	51.9% Score 556.2 DB 9 Length 907;
		Best Local Similarity	87.6% Pred.No.2.9e-126;
		Matches 567; Conservative 31; Mismatches 49; Indels 0; Gaps 0.	
OY	426	AGACTCTTGGGAGAAGACCCCACTGTGAAGTCATGAGCATTAGGCCCATANGAA	485
Db	751	ATACTCTTTAATTAATTCACCACCTTAGCTCTTTAATTAATTAATTAATTAATTA	692
OY	486	AGTGCGTAAGGGGCCTTGGAACCCCACTGTGTCAAGTGAAGAGGTCAGACTCCAGATCACAG	545
Db	691	ATTTTTTATTTCTTTTATCCCACAATTTTCTATTTATTAATKAKACCCCCATATCACAK	632
OY	546	CGETCTGTAGGAGAGTCTATCTACTGAAGCGGAGAAGACTTAAACCACCGCTCTCTCC	605
Db	631	CTCTCTTAAKTAAATCTCATCCCATCTAATCTARAKARACTFAAACCCGCKTCTCC	572
OY	606	TCCACACCTCATATCCCGGCCACCTGTGAGGGGCTGACCAAATCCAATCAATGGNCTT	665
Db	571	TTCACACTCATATCCCGGCCACCTGTTRTKRKRCTGACCAATCAATCAATCAATGRTGCTT	512
OY	666	CAAAAGGAGAGACCCAGTACTCTCTCTCTCTTACTCTTAATSCAATGGTCCCATCATTC	725
Db	511	CAAAAAGGAGAGACCCAGTACTCTCTCTCTCTTACTCTTAATSCAATGGTCCCATCATTC	452
OY	726	TTTGCGGGAAAAATTTCTAGTATTTTGATTAATTTGAATCTTAACCTTCAAGAACCAATAGAACT	785
Db	451	TTTGTGGGGAAAAATTTCTWTATTTTGATTAATTTGAATCTTCAAGAACCAATAGAACT	392
OY	786	CCTGGCCATGAGCTCTTGACCAAGTGAATACACAGCGGATGAGCAACTCTGGCCACA	845
Db	391	CCTGGCCATTAAGACTCTTGACCAAGTGAATMCCMGCCGACACGACACTCTTGGCCMACA	332
OY	846	AAAATGTGTGCAATAGAAAGTATATCAAGCAATATATCCACACCAAGGCTTCTGTAA	905
Db	331	AAAATKTGTGCAATAGAAAGTATATCAAGCAATATATCCACACCAAGGCTTCTGTAA	272
OY	906	CTGGGACCAATGATTAATCTCATAGGCGCTGTTGTGAGATTAGATGAATTAACCTGTGAAA	965

Db	271	CTGGAGCAAAATGATTACCTCAATGAGGCGCTGTGTGAGATTATGAGTAAGAAATACCGTGA	212
QY	966	GTGCGCTTAGCAGTGCACGCCAAATAGAGGCGATTCATGAACATTTTTCATATATAACC	1025
Db	211	GTGCGCTTAGCAGTGCACGCCAAATAGAGGCGATTCATGAACATTTTTCATATATAAAC	152
QY	1026	AAAAAATACCTGTATATCAATATAAAACCTTGCATCCATCATGAATTTTC	1072
Db	151	AAAAAATACCTGTATATCAATATAAAACCTTGCATCCATCATGAATTTTC	105
RESULT	12		
LOCUS	AM957082	625 bp	mRNA linear EST 01-JUN-2000
DEFINITION	EST369152 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence.		
ACCESSION	AM957082		
VERSION	AM957082.1	GI:8146765	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Hegde,P., Qi,R., Abernathy,K., Dharp,S., Gaspard,R., Gay,C., Holt ,I.E., Seed,A.L., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.		
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johng@tigr.org Plate: 101		
FEATURES	Seq primer: Reverse.		
source	Location/Qualifiers		
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	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone_lib="MAGE resequences, MAGD"		
	/note="Vector: p BluescriptSKm"		
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Best Local Similarity	99.6%;	Pred. No. 3.2e-18;	Length 625;
Matches 557;	Conservative 0;	Mismatches 2;	Indels 0;
			Gaps 0;
QY	514	GTCCAGTGGAGAGGTCACACTCCACATATACAGCGCTCGGAGGAGTCTATCTACTGAA	573
Db	1	GTCACTGAGAGAGGTCACACCCCGACATATACACGCTCTGAGGAAGTCTATCTACTGAA	60
QY	574	GCGAGAAAGACTTATTAACCAACGCGCTCTCTCCCTCCACACCTCATCCGCCACCTGTGT	633
Db	61	GCGAGAAAGACTTATTAACCAACGCGCTCTCTCCCTCCACACCTCATCCGCCACCTGTGT	120
QY	634	GGGCGTGCACATATGCAAACTCAATATGGTCTTCAAAAGGAGAGACCCACTGACTCTCTT	693
Db	121	GGGCGTGCACATATGCAAACTCAAAATGGTCTTCAAAAGGAGAGACCCACTGACTCTCTT	180
QY	694	CCTTACCTTATATGCAATTTGGTCCCATCATCTTGTGGGGGGAATAATCTAGATTTTGA	753
Db	181	CCTTACCTTATATGCAATTTGGTCCCATCATCTTGTGGGGGGAATAATCTAGATTTTGA	240
QY	754	TTATTTGAATCTTACAGCAACAAATAGGAACCTCTGGCCAATGAGAGCTCTTGACACAGT	813
Db	241	TTATTTGAATCTTACAGCAACAAATAGGAACCTCTGGCCAATGAGAGCTCTTGACACAGT	300
QY	814	AATCAACAGCCGATATGCAAGCTCTTGCCAACAAAATGTGTGGCAAAATGAGATATATCA	873

Db 301 AATCACCAGCCGATACGACGCTTGGCCAAACAAATGTGTGCAATAGATATATCA 360  
Qy 874 AGCAATATATCCACCCAGGCTTGTGTAACTGGGACCAATATATCTCATAGGCT 933  
Db 361 AGCAATATATCTCCACCCAGGCTTGTGTAACTGGGACCAATATATCTCATAGGCT 420  
Qy 934 GTGTGTAGATTTAGATGAATAATACCTGTGAAGTGCCTAGGACAGTGCACCAATAGGA 993  
Db 421 GTGTGTAGATTTAGATGAATAATACCTGTGAAGTGCCTAGGACAGTGCACCAATAGGA 480  
Qy 994 GGCATTAAATGACATTTTGTGATATAAACCAAAAAATTAATCTGTATCAATAAAACT 1053  
Db 481 GGCATTAAATGACATTTTGTGATATAAACCAAAAAATTAATCTGTATCAATAAAACT 540  
Qy 1054 TGCATCCACATGATTTTC 1072  
Db 541 TGCATTCACATGATTTTC 559

RESULT 13  
BE314194 534 bp mRNA linear EST 26-OCT-2000  
LOCUS 601152806F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:3509112 5',  
DEFINITION mRNA sequence.  
ACCESSION BE314194  
VERSION BE314194  
KEYWORDS GI:9135018  
SOURCE EST.  
ORGANISM human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 534)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapds@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: Image.Lnl.gov  
Plate: LNCMI91 row: K column: 01  
High quality sequence stop: 534.  
Location/Qualifiers  
1..534  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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/lab\_host="DH10B (phage-resistant)"  
/note="Organ: brain; Vector: pORF7; Site1: XhoI; Site2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

BASE COUNT 111 a 161 c 165 g 97 t  
ORIGIN

Query Match 49.5%; Score 530.8; DB 10; Length 534;  
Best Local Similarity 99.6%; Pred. No. 4.3e-120;  
Matches 532; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 18 AACAAAGCCATGTGGCGGACGAGCGGCTGCTCCGTGGGCGGCGCT 77  
Db 1 AACAAAGCCATGTGGCGGACGAGCGGCTGCTCCGTGGGCGGCGCT 60

Qy 78 GCGGAGACGAGGACGAGGACTTACAGCTTCAAGGCGGTCACATCCGGGCAAACTGG 137  
Db 61 GCGGAGACGAGGACGAGGACTTACAGCTTCAAGGCGGTCACATCCGGGCAAACTGG 120  
Qy 138 TGTGCTGGAGAGTACCGCGGATCGGTGCTGTGTGATGTGGCCAGGAGTGGG 197  
Db 121 TGTGCTGGAGAGTACCGCGGATCGGTGCTGTGTGATGTGGCCAGGAGTGGG 180  
Qy 198 GCTTCACAGACGACACTACCGAGCCCTGACGAGCTGCAGGAGACTGGGCCACC 257  
Db 181 GCTTCACAGACGACACTACCGAGCCCTGACGAGCTGCAGGAGACTGGGCCACC 240  
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RESULT 14  
AM959644 542 bp mRNA linear EST 01-JUN-2000  
LOCUS EST371714 MAGE resequences, MAGF Homo sapiens cDNA, mRNA sequence.  
ACCESSION AM959644  
VERSION AM959644.1 GI:8149328  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 542)  
Hedge, P., Qi, R., Ahernathy, K., Dharap, S., Gaspar, R., Gay, C., Holt  
, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and  
Quackenbush, J.  
Assessment of gene expression patterns in a model of colon tumor  
metastasis using a 19,200 element cDNA microarray  
Unpublished (2000)  
Contact: John Quackenbush  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 3528  
Fax: 301 838 0208  
Email: johnq@igf.org  
Plate: 135  
Seq primer: Forward.  
Location/Qualifiers  
1..542  
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/clone\_image="MAGE resequences, MAGF"  
/note="Vector: pBluescriptSm"

BASE COUNT 117 a 161 c 161 g 103 t  
ORIGIN

Query Match 47.6%; Score 510.8; DB 9; Length 542;  
Best Local Similarity 97.6%; Pred. No. 3.7e-115;  
Matches 529; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

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/lab_host="DH10B"
/notes="Organ: mixed (see below); Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHMP, pregnant uterus NbHMPu, and fetal heart NbH19M) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT      131 a      100 c      126 g      162 t
ORIGIN

Query Match      47.6%; Score 510.4; DB 9; Length 519;
Best Local Similarity 99.8%; Pred. No. 4.5e-115;
Matches 511; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 556 GAAGCTCATCTCTAGCGAAGCGGAAAGACTTTAAACACCGGGGTCCCTCCACACACCT 615
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QY 616 CATCCCGCCACACTGTGTGGGGCTGACCAATGCAAACTCAAAATGGTGCTTCAAGGAGA 675
Db 452 CATCCCGCCACACTGTGTGGGGCTGACCAATGCAAACTCAAAATGGTGCTTCAAGGAGA 393
QY 676 GACCCACAGACTCCCTCTCTACTCTTATGCCATTTGGTCCCATCATTTTGGGGAGA 735
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QY 736 AAAATTCTAGATTTTGGATTTTGGAACTTACAGCAACAAATAGGAACCTCTGGCCAA 795
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